

## FIGURE 168

GTGGAGGCCGCCGACGATGGCGGGGCCGACGGAGGCCGAGACGGGGTTGGCCGAGCCCCGGG  
CCCTGTGCGCGCAGCGGGGCCACCGCACCTACGCGCGCCGCTGGGTGTTCTGTCTCGCGATC  
AGCCTGCTCAACTGCTCCAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTCAT  
TGCTGAGGACTTGGTCCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTGG  
TATCCACCCCATTTGGCGTGGCGGCCATCTGGATCCTGGACTCCGTCGGGCTCCGTGCGGCG  
ACCATCCTGGGTGCGTGGCTGAACTTTGCCGGGAGTGTGCTACGCATGGTGCCCTGCATGGT  
TGTTGGGACCCAAAACCCATTTGCCTTCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC  
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGCTGCCTTGTGGTTCCCAGAGCACCAGCGA  
GCCACGGCCAACATGCTCGCCACCATGTGGAACCTCTGGGCGTCTTGTGGCCAATGTGCT  
GTCCCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCCGTTAATGCTCGGTGTCTATACCATCC  
CTGCTGGCGTCTGCTGCCTGCTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCACCCCCG  
CCCTCTGCCGGGGCTGCCAGCTCCACCTCAGAGAAAGTTCTTGATGGGCTCAAGCTGCAGCT  
CATGTGGAACAAGGCCTATGTCTATCCTGGCTGTGTGCTTGGGGGGAATGATCGGGATCTCTG  
CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTTCC  
GGCCTCTGTGGCGCTCTCTTCATCACGTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCTTA  
TGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCTGTTCTCTCTGG  
CCTGCGTGCCCTTTGCCCTGGTGTCCAGCTGCAGGGACAGACCCTTGCCCTGGCTGCCACC  
TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTCTGA  
GTGTTCCCTTCCCCGTGGGGGAGGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG  
AGGGAATACTCATCATGCTGGCAATGACGGCACTGACTGTGCGACGCTCGGAGCCGTCTTG  
TCCACCTGCCAGAGGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGCTGATGGCCGG  
CCTGTGCACCTTCTTCAGCTGCATCCTGGCGGTCTTCTTCCACACCCCATACCGGCGCCTGC  
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAACGCCGTGGGCGGCGCAGACTCAGGGCCG  
GGTGTGGACCGAGGGGGAGCAGGAAGGGCTGGGGTCTTGGGGCCCAGCACGGCGACTCCGGA  
GTGCACGGCGAGGGGGGCTCGCTAGAGGACCCAGAGGGCCCGGAGCCCCACCCAGCCT  
GCCACCGAGCGACTCCCCGTGCGCAAGGCCAGCAGCCACCGACGCGCCCTCCCGCCCCGGC  
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCCGGCTGGGTCTCACTCCTCCTT  
CTCCTCCCCGTGGGTGATCACGTAGCTGAGCGCCTTGTAAGTCCAGGTTGCCCGCCACATCGA  
TGGAGGCGAACTGGAACATCTGGTCCACCTGCGGGCGGGGGCGAAAGGGCTCCTTGCGGGCT  
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

0973295-101501

## **FIGURE 169**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988

><subunit 1 of 1, 560 aa, 1 stop

><MW: 58427, pI: 6.86, NX(S/T): 2

MAGPTEAETGLAEPRALCAQRGHRITYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV  
LSMEQINWLSLVYLVVSTPFGVAAIWILDSVGLRAATILGAWLNFAGSVLRMVPCMVVGTQN  
PFAFLMGGQSLCALAQSLVIFSPAKLAALWFPEHQRATANMLATMSNPLGVLVANVLSPLV  
KKGEDIPLMLGVYTIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA  
YVILAVCLGGMIGISASFSALLEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK  
HFTEATKIGLCLFSLACVPFALVSQLOGQTLALAATCSLLGLFGFSVGPVAMELAVECSFPV  
GEGAATGMIFVLGQAEGLIMLAMTALTVRREPSLSTCQQGEDPLDWTVSLLLMAGLCTFF  
SCILAVFFHTPYRRLQAESGEPPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG  
ASLEDPRGPGSPHPACHRATPRAQGPAATDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPWVIT

### **Important features:**

#### **Signal peptide:**

amino acids 1-44

#### **Transmembrane domains:**

amino acids 61-79, 98-112, 126-146, 169-182, 201-215, 248-268,  
280-300, 318-337, 341-357, 375-387, 420-441

#### **N-glycosylation site.**

amino acids 40-43 and 43-46

#### **Glycosaminoglycan attachment site.**

amino acids 468-471

## FIGURE 170

GTCCACATCCTGCTCAACTGGGTGAGTCCCTCTTAGACCAGCTCTTGTCATCATTTGCTGAAGTGGACCAAC  
 TAGTTCCCCAGTAGGGGGTCTCCCTGGCAATTCTTGATCGGCGTTTGGACATCTCAGATCGCTTCCAATGAAGA  
 TGGCCTTGCTTGGGGTCTGCTTGTTCATAATCATCTAACTATGGGACAAGGTTGTGCCGGCAGCTCTGGGGG  
 AAGGAGCACGGGGTGTATCAAGCCATCCAGGAAACACTGGAGGACTTGTCCAGCCTTGAAAGAACCTCTAGTGGTT  
 TCTGAATCTAGCCACTTGGCGGTAAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGGTGG  
 CTACTTATTTCTTTTAGGGGATTGTGAGGAGTGACCACTCTCACGGTGAAATACCAAGTGTGAGAGGAAGTGCC  
 ATCTGGTACAGTGATCGGGAAGCTGTCCAGGAAGTGGGCCGGGAGGAGAGGCGGAGGCAAGCTGGGGCCGCCTT  
 CCAGGTGTTGAGCTGCCTCAGGCGCTCCCAATTAGGTGGACTCTGAGGAAGGCTTGCTCAGCACAGGCAAGCG  
 GCTGGATCGAGAGCAGCTGTGCCGACAGTGGGATCCCTGCCTGGTTTCTTTGATGTGCTTGCCACAGGGGATTT  
 GGCTCTGATCCATGTGGAGATCCAAGTGTGGACATCAATGACCACCAGCCACGGTTTCCAAAGGCGAGCAGGA  
 GCTGGAAATCTCTGAGAGCGCCTCTCTGCGAACCCGGATCCCCCTGGACAGAGCTCTTGACCCAGACACAGGCC  
 TAACACCCTGCACACCTACACTCTGTCTCCAGTGAGCACTTTGCCTTGGATGTATTGTGGGCCCTGATGAGAC  
 CAAACATGCAGAACTCATAGTGGTGAAGGAGCTGGACAGGGAATCCATTCATTTTTGTATCTGGTGTAACTGC  
 CTATGACAATGGGAACCCCCCAAGTCAAGTACAGCTTGGTCAAGGTCAACGTCTTGGAATCCAATGACAATAG  
 CCCTGCGTTTGTGAGAGTTCACTGGCACTGGAAATCCAAGAAGATGCTGCACCTGGTACGCTTCTCATAAACT  
 GACCGCCACAGCCCTGACCAAGGCCCAATGGGAGGTGGAGTTCTTCTCAGTAAGCACATGCCCTCAGAGGT  
 GCTGGACACCTTCAGTATTGATGCCAAGACAGGCAAGGTCACTTCTGCGTGCAGCTCTAGACTATGAAAAGAACC  
 TGCTTACGAGGTGGATGTTGAGGCAAGGACCTGGGTCCCAATCCTATCCAGCCCATGCAAAGTTCTCATCAA  
 GGTTCCTGGATGTCAATGACAACATCCCAAGCATCCAGTCAATGGGCCCTCCAGCCATCACTGGTGTGAGAAGC  
 TCTTCCCAAGGACAGTTTATTGCTCTTGTCTATGGCAGATGACTTGGATTGAGGACACAATGGTTTGGTCCACTG  
 CTGGCTGAGCCAAAGAGCTGGGCCACTTCAGGCTGAAAAGAACTAATGGCAACACATACATGTTGCTAACCATG  
 CAGCTGTGACAGAGCAGTGGGCCAAATATACCTCACTCTGTTAGCCCAAGACCAAGGACTCCAGCCCTTATC  
 AGCCAAGAAACAGCTCAGCATTAGATCAGTGACATCAACGACAATGCACCTGTGTTTGAAGAAAGCAGGTATGA  
 AGTCTCCAGCGGGGAAAACAACCTTACCTCTCTTCACTCATTACCATCAAGGCTCATGATGCAGACTTGGGCAT  
 TAATGGAAAAGTCTCATACCGCATCCAGGACTCCCACTTGTCTCACTTAGTAGCTATTGACTCCAACACAGGAGA  
 GGTCACTGCTCAGAGGTCACTGAACATATGAAGAGATGGCCGGCTTTGAGTTCCAGGTGATCGCAGAGGACAGCG  
 GCAACCCATGCTTGATCCAGTGTCTCTGTGTGGGTGAGCCTCTTGGATGCCAATGATAATGCCCCAGAGGTGGT  
 CCAGCCTGTGCTCAGCGATGGAAAAGCCAGCCTCTCGGTGCTTGTGAATGCCTCCACAGGCCACCTGCTGGTGGC  
 CATCGAGACTCCCAATGGCTTGGGCCAGCGGGCACTGACACACCTCCACTGGCCACTCACAGCTCCCGGCCATT  
 CCTTTTGACAACCATTTGTGGCAAGAGATGCAGACTCGGGGGCAAATGGAGAGCCCTCTACAGCATCCGCAATGG  
 AAATGAAGCCCACCTCTTCATCCTCAACCTCATACGGGGCAGCTGTTCGTCAATGTACCAATGCCAGCAGCCT  
 CATTGGGAGTGAGTGGGAGCTGGAGATAGTAGAGGACCAGGGAAGCCCCCTTACAGACCCGAGCCCTGTT  
 GAGGGTCATGTTTGTCAACAGTGTGGACCACCTGAGGGACTCAGCCCGCAAGCCTGGGGCCTTGAGCATGTGAT  
 GCTGACGGTGATCTGCCTGGCTGTACTGTTGGGCATCTTCGGGTGATCCTGGCTTTGTTTCACTGCTCATCTGCCG  
 GACAGAAAAGAAGGACAACAGGGCCTACAACCTGTGGGAGGCCGAGTCCACCTACCGCCAGCAGCCCAAGAGGCC  
 CCAGAAAACATTCAGAAGGCAGACATCCACCTCGTGCCTGTGCTCAGGGGTGAGGAGGTGAGCCTTGTGAAGT  
 CGGGCAGTCCCAAAAGATGTGGACAAGGAGGCGATGATGGAAGCAGGCTGGGACCCCTGCCTGCAGGCCCTT  
 CCACCTCACCCGACCCTGTACAGGACGCTGCGTAATCAAGGCAACCAGGGAGCACCGGCGGAGAGCCGAGAGGT  
 GCTGCAAGACACGGTCAACCTCTTTTCAACCATCCAGGCAGAGGAATGCCTCCCGGGAGAACCCTGAACCTTCC  
 CTGACCCAGCCTGCCACAGGCCAGCCACGTTCCAGGCCCTGAAGGTGTCAGGCAGCCCAAGGGAGGCTGGC  
 TGGAGACCAGGGCAGTGAGGAAGCCCCACAGAGGCCACAGCCTCCTCTGCAACCTGAGACGGCAGCGACATCT  
 CAATGGCAAAGTGTCCCCTGAGAAAGAATCAGGGCCCCGTGAGATCCTGCGGAGCCTGGTCCGGCTGTCTGTGGC  
 TGCCTTGCCTGAGCGGAACCCCGTGGAGGAGCTCACTGTGGATTCTCCTCCTGTTGAGCAAATCTCCAGCTGCT  
 GTCCTTGCTGCATCAGGGCCAATTCCAGCCCAAACCAAACACCGAGGAAATAAGTACTTGGCCAAGCCAGGAGG  
 CAGCAGGAGTGAATCCAGACACAGATGGCCCAAGTGCAAGGGCTGGAGGCCAGACAGACCCAGAACAGGAGGA  
 AGGGCCTTTGGATCCTGAAGAGGACCTCTCTGTGAAGCAACTGCTAGAAGAAGAGCTGTCAAGTCTGCTGGACCC  
 CAGCACAGGTCTGGCCCTGGACCGGCTGAGCGCCCCGTGACCCGGCTGGATGGCGAGACTCTCTTTGCCCTCAC  
 CACCAACTACCGTGACAATGTGATCTCCCCGATGCTGCAGCCACGGAGGAGCCGAGGACCTTCCAGACGTTCCG  
 CAAGGCAGAGGCACAGAGCTGAGCCCAACAGGCACGAGCTGGCCAGCACCTTTGTCTCGGAGATGAGCTCACT  
 GCTGGAGATGCTGCTGGAACAGCGCTCCAGCATGCCCGTGGAGGCCGCTCCGAGGCGCTGCGGCGGCTCTCGGT  
 CTGCGGGAGGACCTCAGTTTAGACTTGGCCACAGTGACGCTCAGGCATGAAAGTGCAAGGGGACCCAGGTGG  
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 CGGCGGCTGAGAATTTAGGGTGACTGATGCTACCCCAACAGAGGAGGCAAGAGCCCCAGGACTAACAGCTGAC  
 TGACCAAAGCAGCCCCCTGTAAAGCAGCTCTGAGTCTTTTGGAGGACAGGGACGGTTTGTGGCTGAGATAAGTGT  
 TCCTGGCAAAACATATGTGGAGCACAAGGGTCACTCCTCTGGCAGAACAGATGCCACGGAGTATCACAGGCAGG  
 AAAGGGTGGCCTTCTTGGGTAGCAGGAGTCAAGGGGCTGTACCTGGGGGTGCCAGGAAATGCTCTCTGACCTAT  
 CAATAAAGGAAAAGCAGTAAAAA